

Amendments to the Claims:

This listing of claims will replace all prior versions, and listings, of claims in the application:

Listing of Claims:

1. (currently amended) A protein interaction system comprising:

a plurality of bait fusion proteins, each fusion protein comprising:

a first ~~fluorogenic~~ fragment of fluorescent protein wherein the fragment is provided by splitting the fluorescent protein at a site(s) to form complementary fragments such that when complementary fragments of the fluorescent protein are functionally associated with each other, a fluorescent signal capable of being detected is generated,

a first peptide of interest wherein the first peptide of interest of each bait fusion protein is identical to the first peptide of interest in each of the other bait fusion proteins, and

a linker portion interposed between the first peptide and first ~~fluorogenic~~ fragment; wherein the linker portions of at least two each bait fusion ~~protein~~ proteins are of different lengths ~~and comprise comprising~~ multiples of the pentapeptide sequence GGGGS (SEQ ID NO:1) ~~glycyl-glycyl-glycyl-glycyl-serine~~, and

at least one prey fusion protein comprising:

a ~~fluorogenic~~ fragment of the fluorescent protein complementary to said first ~~fluorogenic~~ fragment of fluorescent protein,

a second peptide of interest, and

a second linker portion interposed between the complementary ~~fluorogenic~~ fragment and the second peptide wherein the second linker ~~portion~~ portions ~~of each prey fusion protein are of different lengths comprising~~ comprises multiples of the pentapeptide sequence GGGGS (SEQ ID NO:1) ~~glycyl-glycyl-glycyl-glycyl-serine~~;

wherein, on interaction of the first peptide of interest with the second peptide of interest, the ~~fluoregenic~~ fragments of the fluorescent protein functionally associate to promote fluorescence.

2. (canceled)
3. (previously presented) The protein interaction system as claimed in claim 1 wherein at least one linker portion comprises at least 20 amino acids.
4. (previously presented) The protein interaction system according to claim 1, wherein the fragments of fluorescent protein are generatable through the introduction of a split point between the amino acids at positions 157 and 158, or between the amino acids at positions 172 and 173 of the humanised form of Green Fluorescent Protein (SEQ ID NO 2).
5. (previously presented) The protein interaction system as claimed in claim 1, wherein the system comprises a plurality of prey fusion proteins.
6. (original) The protein interaction system as claimed in claim 5 wherein the linker portions of at least two prey fusion proteins are of different lengths.
7. (previously presented) The protein interaction system as claimed in claim 5 wherein at least two of the second peptides of interest of the prey fusion proteins are provided by different amino acid sequences.
8. (currently amended) The protein interaction system as claimed in claim 1, wherein the first peptide is linked to the N terminus of the first ~~fluoregenic~~ fragment of fluorescent protein.
9. (currently amended) The protein interaction system as claimed in claim 1, wherein the first peptide is linked to the C terminus of the first ~~fluoregenic~~ fragment of fluorescent protein.

10. (currently amended) The protein interaction system as claimed in claim 1, wherein the second peptide is linked to the N terminus of the complementary ~~fluorogenic~~ fragment of fluorescent protein.
11. (currently amended) The protein interaction system as claimed in claim 1, wherein the second peptide is linked to the C terminus of the complementary ~~fluorogenic~~ fragment of fluorescent protein.
12. (currently amended) The protein interaction system as claimed in claim 1, further comprising at least a third fusion protein comprising at least a third fragment of fluorescent protein complementary to a first and / or second complementary fragment of fluorescent protein; wherein said at least third fragment is linked to at least a third peptide of interest and at least a third linker is interposed between the at least third fragment and at least third peptide of interest wherein the at least third fragment of fluorescent protein is capable of functional association with a first and / or complementary ~~fluorogenic~~ fragment of fluorescent protein such that on functional association of said fragments fluorescence is enabled and on interaction of the first, second and third peptides of interest the fragments functionally complement each other to promote fluorescence, wherein the at least third linker of the at least third fusion protein comprises multiples of the pentapeptide sequence GGGGS (SEQ ID NO:1) ~~glyeyl-glyeyl-glyeyl-glyeyl-serine~~.
13. (previously presented) A protein interaction system as claimed in claim 1, wherein the system is a cell based system.
14. (withdrawn; currently amended) A library of nucleic acid constructs comprising a plurality of nucleic acid constructs, each construct encoding
(i) a first fragment of fluorescent protein capable of functional association with a complementary fragment of fluorescent protein such that on functional association of said first and complementary fragments fluorescence is enabled,

(ii) a peptide of interest and
(iii) a linker portion, comprising oligonucleotides encoding repeating pentapeptide sequences GGGGS (SEQ ID NO:1) ~~(GGGGS)~~, interposed between the peptide and first fragment of fluorescent protein; wherein the peptide of interest encoded by each nucleic acid construct is the same and the linker portion encoded by each construct is of a different length to the linker encoded by each other construct.

15. (withdrawn) The library according to claim 14, wherein the linker portions comprise in the range 5 to 100 amino acid residues.

16. (withdrawn) The library as claimed in claim 14 wherein at least one linker portion comprises at least 20 amino acids.

17. (withdrawn) The library according to claim 14 wherein the fragments of fluorescent protein are generatable through the introduction of a split point between the amino acids at positions 157 and 158, or between the amino acids at positions 172 and 173 of the humanised form of Green Fluorescent Protein (SEQ ID NO 2).

18. (withdrawn) An expression vector comprising at least one of the plurality of nucleic acid constructs as defined in claim 14, wherein the at least one nucleic acid construct encodes a fusion protein having a linker of at least 20 amino acids.

19. (withdrawn) An expression vector comprising a plurality of nucleic acid constructs as defined in claim 14.

20. (withdrawn) The expression vector according to claim 19, wherein at least one nucleic acid construct encodes a fusion protein having a linker of at least 20 amino acids.

21. (withdrawn) A cell transformed with a vector as claimed in claim 18.

22. (withdrawn) A cell comprising a protein interaction system as claimed in claim 1.
23. (withdrawn) The cell according to claim 22, wherein the cell is transformed with a vector according to claim 18.
24. (withdrawn) An assay method for monitoring peptide interaction comprising the steps of:
(i) providing the protein interaction system of claim 1;
(ii) allowing the bait fusion proteins to come into contact with the prey fusion protein(s); and
(iii) measuring fluorescence produced by the interaction of a first and second peptide of interest causing fragments of the fluorescent protein to functionally interact.
25. (withdrawn) The assay method according to claim 24, wherein the assay is a cell-based assay.
26. (withdrawn; currently amended) The assay method according to claim 24, wherein the cell based assay is performed using one or more cells which have been transformed with a vector comprising a plurality of nucleic acid constructs, wherein each construct encodes:
i) a first ~~fluorogenic~~ fragment of fluorescent protein wherein the fragment is provided by splitting the fluorescent protein at a site(s) to form complementary fragments such that when complementary fragments of the fluorescent protein are functionally associated with each other a fluorescent signal capable of being detected is generated;
ii) a first peptide of interest wherein the first peptide of interest of each bait fusion protein is identical to the first peptide of interest in each of the other bait fusion proteins; and
iii) a linker portion interposed between the first peptide and first ~~fluorogenic~~ fragment wherein the linker portions of each bait fusion protein are of different lengths comprising multiples of a pentapeptide sequence GGGGS (SEQ ID NO:1) ~~glycyl-glycyl-glycyl-glycyl-~~serine.

27. (withdrawn) The method according to claim 24, wherein the assay further comprises the step of determining the subcellular location of the interaction of the first and second peptides of interest in the at least one cell.

28. (withdrawn) The method according to claim 24, wherein the assay further comprises the step of determining the length of the linker(s) of those fusion proteins which allow the first fragment and complementary fragment of the fluorescent protein to functionally complement each other and enable fluorescence to be detected on interaction of the first and second peptide of interest.

29. (withdrawn) The method according to claim 24, wherein the assay comprises the steps of:

providing a putative interaction modulating agent;

measuring the fluorescence produced in the presence of said putative modulating agent;

comparing the measured fluorescence in the presence of the putative modulating agent with the measured fluorescence in the absence of the putative modulating agent;

wherein a decrease in detection of fluorescence in the presence of the putative modulating agent relative to in the absence of the putative modulating agent is indicative that the putative modulating agent prevents or is an inhibitor of peptide interaction; and wherein an increase in detection of fluorescence in the presence of the putative modulating agent relative to in the absence of the putative modulating agent is indicative that the putative modulating agent promotes or enhances peptide interaction.

30. (withdrawn) A kit comprising a library of nucleic acid constructs according to claim 14 and means to express the constructs.

31. (withdrawn) The kit according to claim 30 which further includes at least one second nucleic acid construct which encodes a complementary fragment of fluorescent protein, a second

peptide of interest and a second linker portion interposed between the complementary fragment and the second peptide of interest.

32. (withdrawn) The kit as claimed in claim 31 wherein the kit comprises a plurality of second nucleic acid constructs, wherein the second peptides of interest encoded by the plurality of second nucleic acid constructs are each of different amino acid sequence.

33. (new) A protein interaction system as claimed in claim 1 wherein at least three different linker lengths are provided.

34. (new) A protein interaction system as claimed in claim 1 wherein at least five different linker lengths are provided.